

SEQUENCE LISTING

<110> Yamanouchi Pharmaceutical Co., Ltd.

<120> Novel potassium-dependent sodium/calcium exchanger

<130> Y0335PCT-693

<150> JP 2002-225114

<151> 2002-08-01

<150> JP 2003-182989

<151> 2003-06-26

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14).. (1882)

<223>

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<223> Inventor: Nozawa, Katsura; Mochizuki, Shinobu

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Val Leu Ala Leu Val Cys Cys Ala Ser Gly Leu Phe Gly Ser Leu Gly	
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His Lys Thr Ala Ser Ala Ser Lys Arg Val Leu Pro Asp Thr Trp Arg
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Asn Arg Lys Leu Met Ala Pro Val Asn Gly Thr Gln Thr Ala Lys Asn
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Cys Thr Asp Pro Ala Ile His Glu Phe Pro Thr Asp Leu Phe Ser Asn
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Lys Glu Arg Gln His Gly Ala Val Leu Leu His Ile Leu Gly Ala Leu
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Tyr Met Phe Tyr Ala Leu Ala Ile Val Cys Asp Asp Phe Phe Val Pro
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Gly Ala Thr Phe Met Ala Ala Gly Ser Ser Thr Pro Glu Leu Phe Ala
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Ser Val Ile Gly Val Phe Ile Thr His Gly Asp Val Gly Val Gly Thr
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Ile Val Gly Ser Ala Val Phe Asn Ile Leu Cys Ile Ile Gly Val Cys
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Pro Gln Pro Pro Pro Pro Glu Pro Glu Pro Val Glu Ala Asp Phe Leu	
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Ser Pro Phe Ser Val Pro Glu Ala Arg Gly Asp Lys Val Lys Trp Val	
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Phe Thr Trp Pro Leu Ile Phe Leu Leu Cys Val Thr Ile Pro Asn Cys	
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575 580 585

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590 595 600

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Ser Ala Ser Lys Arg Val Leu Pro Asp Thr Trp Arg Asn Arg Lys Leu
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Met Ala Pro Val Asn Gly Thr Gln Thr Ala Lys Asn Cys Thr Asp Pro
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Ala Ile His Glu Phe Pro Thr Asp Leu Phe Ser Asn Lys Glu Arg Gln
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His Gly Ala Val Leu Leu His Ile Leu Gly Ala Leu Tyr Met Phe Tyr
 100 105 110

Ala Leu Ala Ile Val Cys Asp Asp Phe Phe Val Pro Ser Leu Glu Lys
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Ile Cys Glu Arg Leu His Leu Ser Glu Asp Val Ala Gly Ala Thr Phe
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Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile Leu Tyr Val Phe
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Gly Arg His Glu Asn Ile Glu Asn Gly Asn Val Pro Val Glu Asn Pro
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Pro Pro Glu Pro Glu Pro Val Glu Ala Asp Phe Leu Ser Pro Phe Ser
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Trp Glu Lys Phe Phe Met Val Thr Phe Ile Thr Ala Thr Leu Trp Ile
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Ala Val Phe Ser Tyr Ile Met Val Trp Leu Val Thr Ile Ile Gly Tyr
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Thr Leu Gly Ile Pro Asp Val Ile Met Gly Ile Thr Phe Leu Ala Ala
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Gly Thr Ser Val Pro Asp Cys Met Ala Ser Leu Ile Val Ala Arg Gln
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Gly Leu Gly Asp Met Ala Val Ser Asn Thr Ile Gly Ser Asn Val Phe
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Asp Ile Leu Val Gly Leu Gly Val Pro Trp Gly Leu Gln Thr Met Val
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Val Asn Tyr Gly Ser Thr Val Lys Ile Asn Ser Arg Gly Leu Val Tyr
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Ser Val Val Leu Leu Leu Gly Ser Val Ala Leu Thr Val Leu Gly Ile
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His Leu Asn Lys Trp Arg Leu Asp Arg Lys Leu Gly Val Tyr Val Leu
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Arg Arg Arg Arg Glu Met Leu Pro Gln Gln Val Gly Phe Val Cys Ala
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Val Leu Ala Leu Val Cys Cys Ala Ser Gly Leu Phe Gly Ser Leu Gly
30 35 40

cac aaa aca gct tct gct agc aaa cgt gtc ctg cca gac aca tgg aga 193
His Lys Thr Ala Ser Ala Ser Lys Arg Val Leu Pro Asp Thr Trp Arg
45 50 55 60

aat aga aag ttg atg gcc cca gtg aat ggg aca cag aca gcc aag aac 241
Asn Arg Lys Leu Met Ala Pro Val Asn Gly Thr Gln Thr Ala Lys Asn
65 70 75

tgc aca gat cct gcg att cac gag ttc ccc aca gat ctg ttc tcc aat 289
Cys Thr Asp Pro Ala Ile His Glu Phe Pro Thr Asp Leu Phe Ser Asn
80 85 90

aag gag cga cag cac gga gcc gtc ctg ctg cac atc ctt ggt gct ctg 337
Lys Glu Arg Gln His Gly Ala Val Leu Leu His Ile Leu Gly Ala Leu
95 100 105

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Gly Ala Thr Phe Met Ala Ala Gly Ser Ser Thr Pro Glu Leu Phe Ala	
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Ser Val Ile Gly Val Phe Ile Thr His Gly Asp Val Gly Val Gly Thr	
160 165 170	
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Arg Asp Ser Val Tyr Tyr Thr Ile Ser Val Ile Val Leu Ile Val Phe	
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Ile Tyr Asp Glu Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile	
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gcc ttt ttc aca gtc aaa caa aag agc att gca aac ggt aac ccg gtc	817
Ala Phe Phe Thr Val Lys Gln Lys Ser Ile Ala Asn Gly Asn Pro Val	
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Asn Ser Glu Leu Glu Ala Val Lys Glu Lys Pro Gln Tyr Gly Lys Asn	
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Pro Val Val Met Val Asp Glu Ile Met Ser Ser Ser Pro Pro Lys Phe	
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ccc agg acc cga cta cgg atg gcc agc agg atc atc att aat gag cgg	1009
Pro Arg Thr Arg Leu Arg Met Ala Ser Arg Ile Ile Ile Asn Glu Arg	
320 325 330	
cag aga ctg atc aac tcg gcc aat ggt gtg agc agt aag ccg ctt caa	1057
Gln Arg Leu Ile Asn Ser Ala Asn Gly Val Ser Ser Lys Pro Leu Gln	
335 340 345	
aac ggg agg cac gag aac att gag aac ggg aat gtt cct gtg gaa aac	1105
Asn Gly Arg His Glu Asn Ile Glu Asn Gly Asn Val Pro Val Glu Asn	
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Pro Leu Ile Phe Leu Leu Cys Val Thr Ile Pro Asn Cys Ser Lys Pro	
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Ile Ala Val Phe Ser Tyr Ile Met Val Trp Leu Val Thr Ile Ile Gly	
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465 470 475	
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Ala Gly Thr Ser Val Pro Asp Cys Met Ala Ser Leu Ile Val Ala Arg	
480 485 490	
caa ggc ctt ggg gac atg gca gtc tcc aac acc ata gga agc aac gtg	1537
Gln Gly Leu Gly Asp Met Ala Val Ser Asn Thr Ile Gly Ser Asn Val	
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Phe Asp Ile Leu Val Gly Leu Gly Val Pro Trp Gly Leu Gln Thr Met	
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Val Val Asn Tyr Gly Ser Thr Val Lys Ile Asn Ser Arg Gly Leu Val	
525 530 535 540	
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Tyr Ser Val Val Leu Leu Leu Gly Ser Val Ala Leu Thr Val Leu Gly	
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 35 40 45

Ser Ala Ser Lys Arg Val Leu Pro Asp Thr Trp Arg Asn Arg Lys Leu
 50 55 60

Met Ala Pro Val Asn Gly Thr Gln Thr Ala Lys Asn Cys Thr Asp Pro
 65 70 75 80

Ala Ile His Glu Phe Pro Thr Asp Leu Phe Ser Asn Lys Glu Arg Gln
 85 90 95

His Gly Ala Val Leu Leu His Ile Leu Gly Ala Leu Tyr Met Phe Tyr
 100 105 110

Ala Leu Ala Ile Val Cys Asp Asp Phe Phe Val Pro Ser Leu Glu Lys
 115 120 125

Ile Cys Glu Arg Leu His Leu Ser Glu Asp Val Ala Gly Ala Thr Phe
 130 135 140

Met Ala Ala Gly Ser Ser Thr Pro Glu Leu Phe Ala Ser Val Ile Gly
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Val Phe Ile Thr His Gly Asp Val Gly Val Gly Thr Ile Val Gly Ser
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Gly Gln Val Val Arg Leu Thr Trp Trp Ala Val Cys Arg Asp Ser Val
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Tyr Tyr Thr Ile Ser Val Ile Val Leu Ile Val Phe Ile Tyr Asp Glu
 210 215 220

Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile Leu Tyr Val Phe
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Tyr Ile Leu Ile Met Lys Tyr Asn Val Lys Met Gln Ala Phe Phe Thr
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Val Lys Gln Lys Ser Ile Ala Asn Gly Asn Pro Val Asn Ser Glu Leu
 260 265 270

Glu Ala Val Lys Glu Lys Pro Gln Tyr Gly Lys Asn Pro Val Val Met
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Val Asp Glu Ile Met Ser Ser Ser Pro Pro Lys Phe Thr Phe Pro Glu
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Ala Gly Leu Arg Ile Met Ile Thr Asn Lys Phe Gly Pro Arg Thr Arg
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Gln Gln Asn Gln Glu Gln Gln Pro Pro Pro Gln Pro Pro Pro Glu
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Pro Glu Pro Val Glu Ala Asp Phe Leu Ser Pro Phe Ser Val Pro Glu
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Ala Arg Gly Asp Lys Val Lys Trp Val Phe Thr Trp Pro Leu Ile Phe
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Leu Leu Cys Val Thr Ile Pro Asn Cys Ser Lys Pro Arg Trp Glu Lys
 420 425 430

Phe Phe Met Val Thr Phe Ile Thr Ala Thr Leu Trp Ile Ala Val Phe
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Ser Tyr Ile Met Val Trp Leu Val Thr Ile Ile Gly Tyr Thr Leu Gly
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Ile Pro Asp Val Ile Met Gly Ile Thr Phe Leu Ala Ala Gly Thr Ser
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Val Pro Asp Cys Met Ala Ser Leu Ile Val Ala Arg Gln Gly Leu Gly
 485 490 495

Asp Met Ala Val Ser Asn Thr Ile Gly Ser Asn Val Phe Asp Ile Leu
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Val Gly Leu Gly Val Pro Trp Gly Leu Gln Thr Met Val Val Asn Tyr
 515 520 525

Gly Ser Thr Val Lys Ile Asn Ser Arg Gly Leu Val Tyr Ser Val Val
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Leu Leu Leu Gly Ser Val Ala Leu Thr Val Leu Gly Ile His Leu Asn
 545 550 555 560

Lys Trp Arg Leu Asp Arg Lys Leu Gly Val Tyr Val Leu Val Leu Tyr
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<210> 6
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<212> DNA

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